

FIG. 1

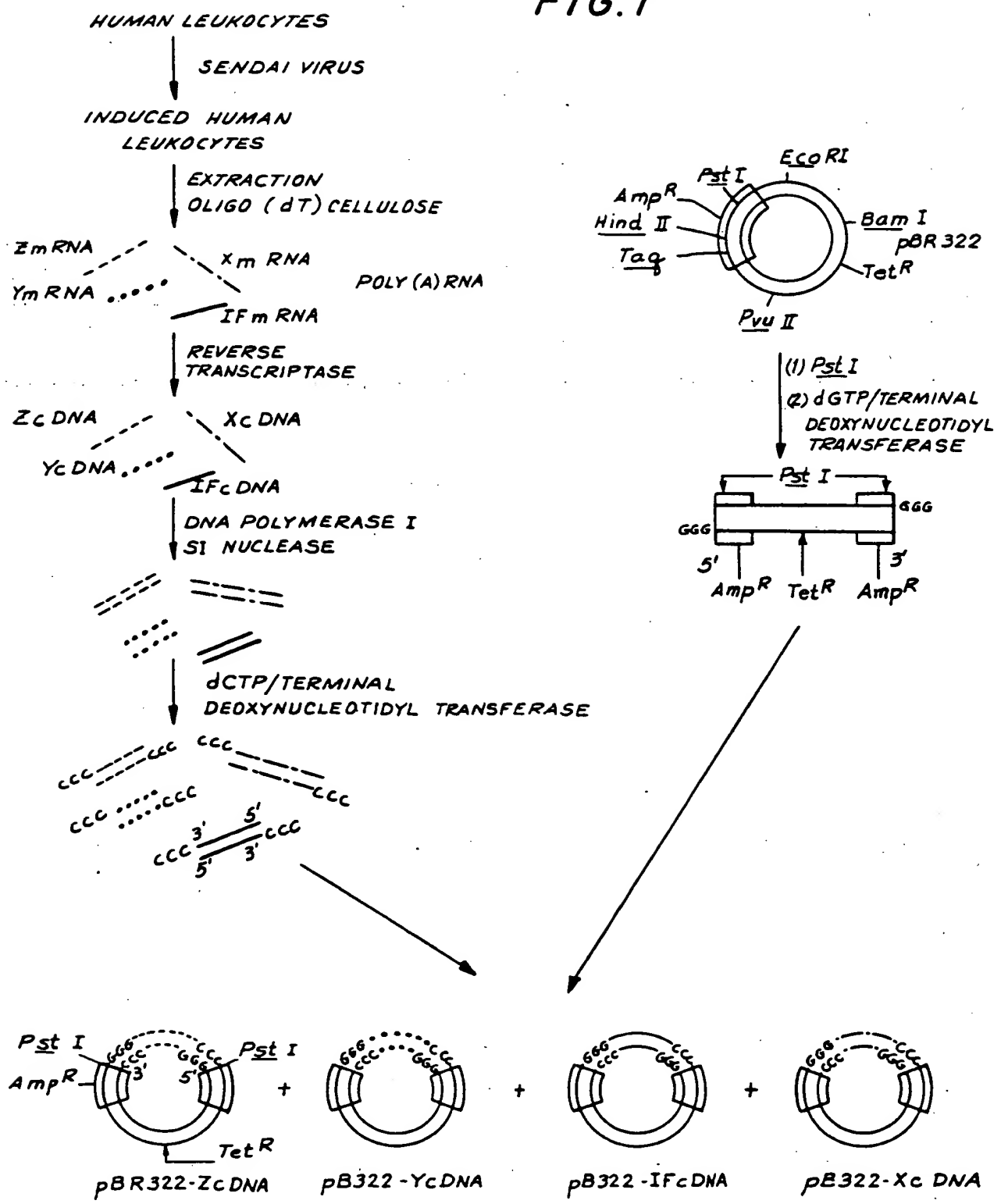


FIG. 2

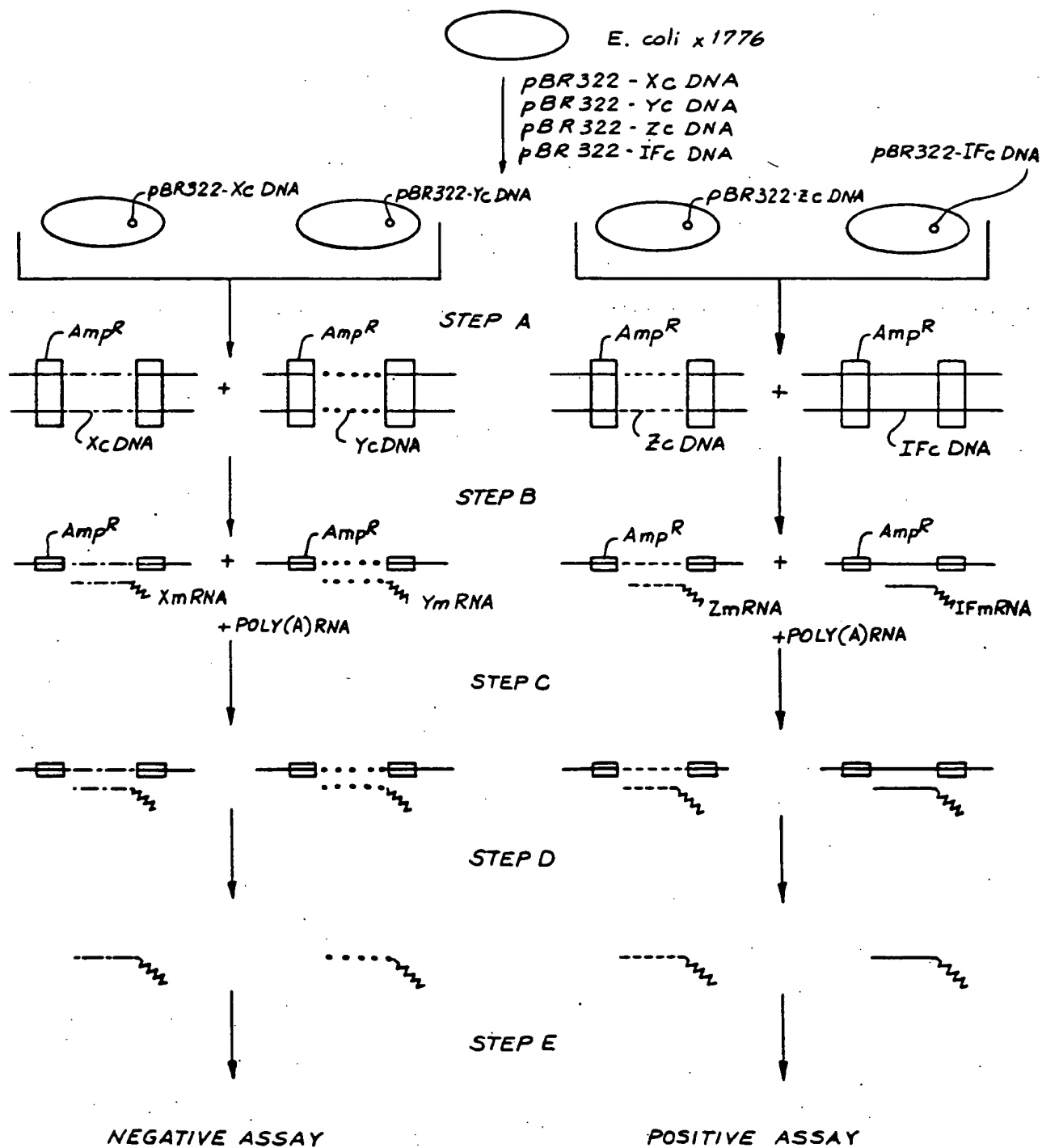


FIG. 3

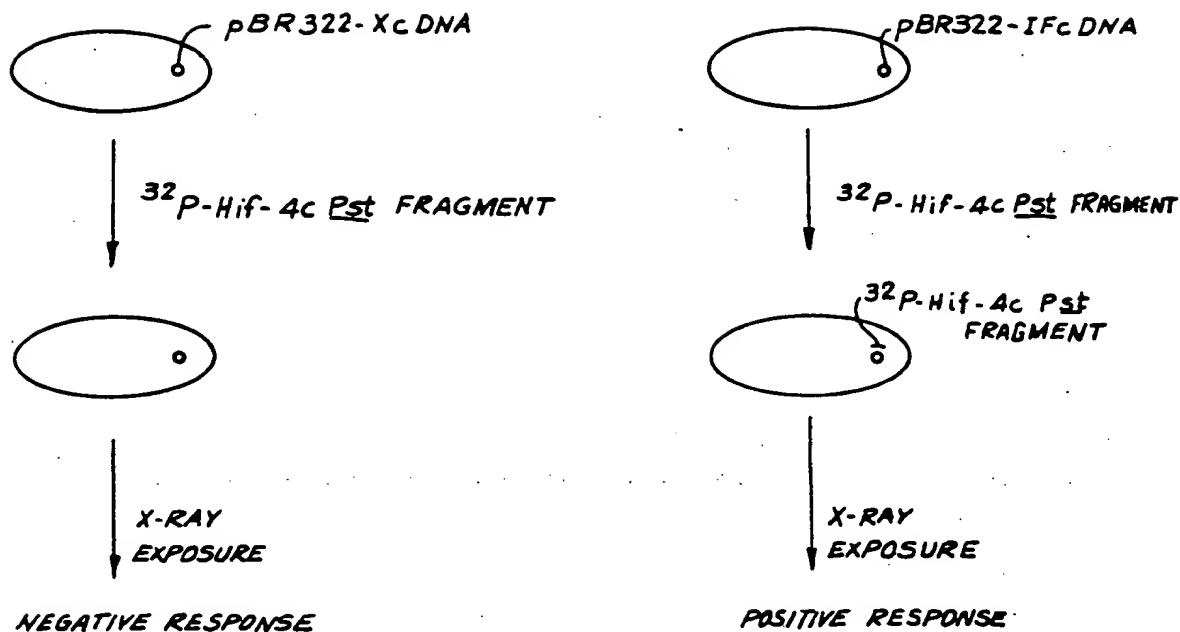


FIG. 4

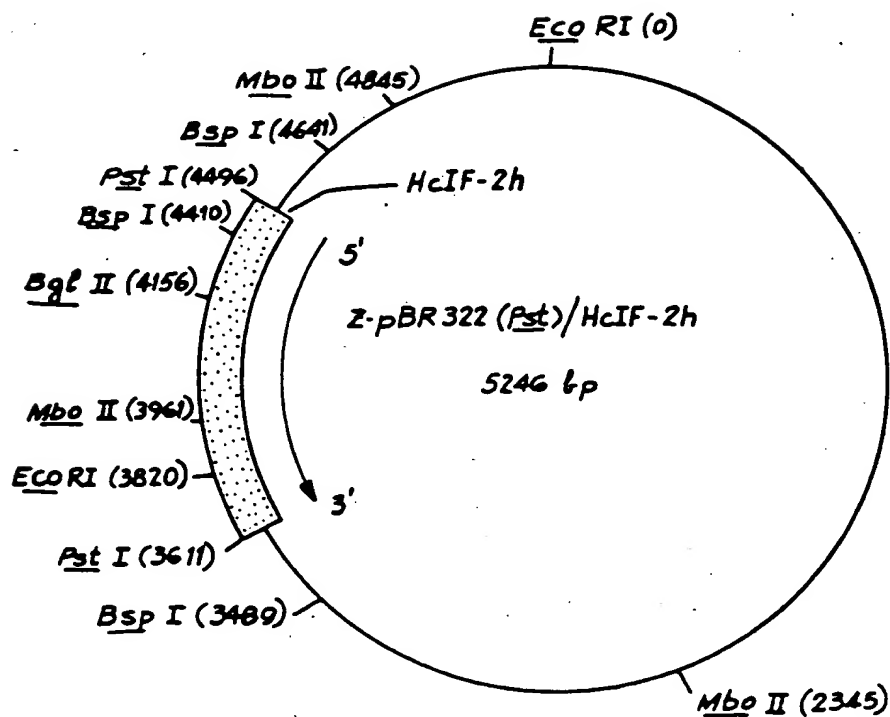
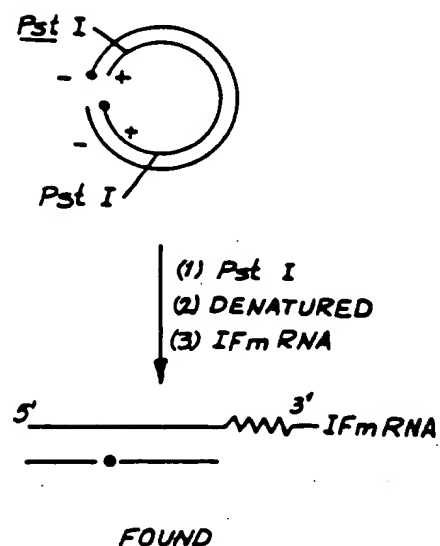
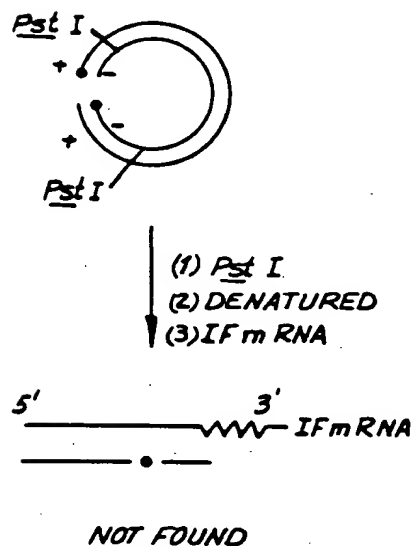
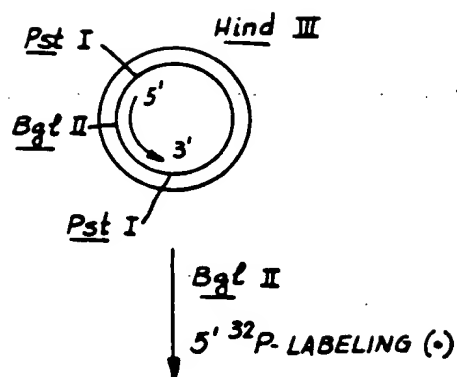
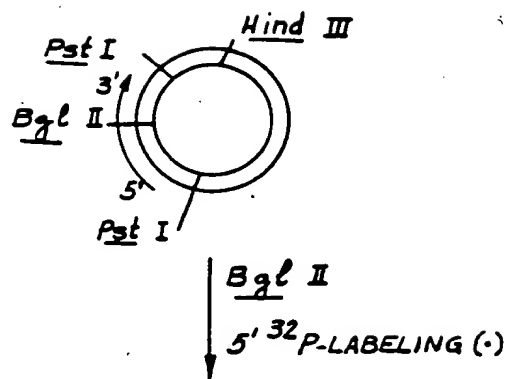


FIG. 5



10  
 MetSerIleGlnHisPheArgValAlaLeuIleProPhePheAlaAlaPheCysLeuProValPheAlaHisProGluThr  
 20  
 pBR322 ATGAGTATTCAACATTTCCGTGTGCCCCATTATCCCTTTTGGGCAATTTTGGCTTCCCTGTTTGTCTACCCAGAAACG  
 181  
 29 LeuVal ProAlaAlaMet  
 CTGGTG...CCTGCAGCAATG...  
 Pat

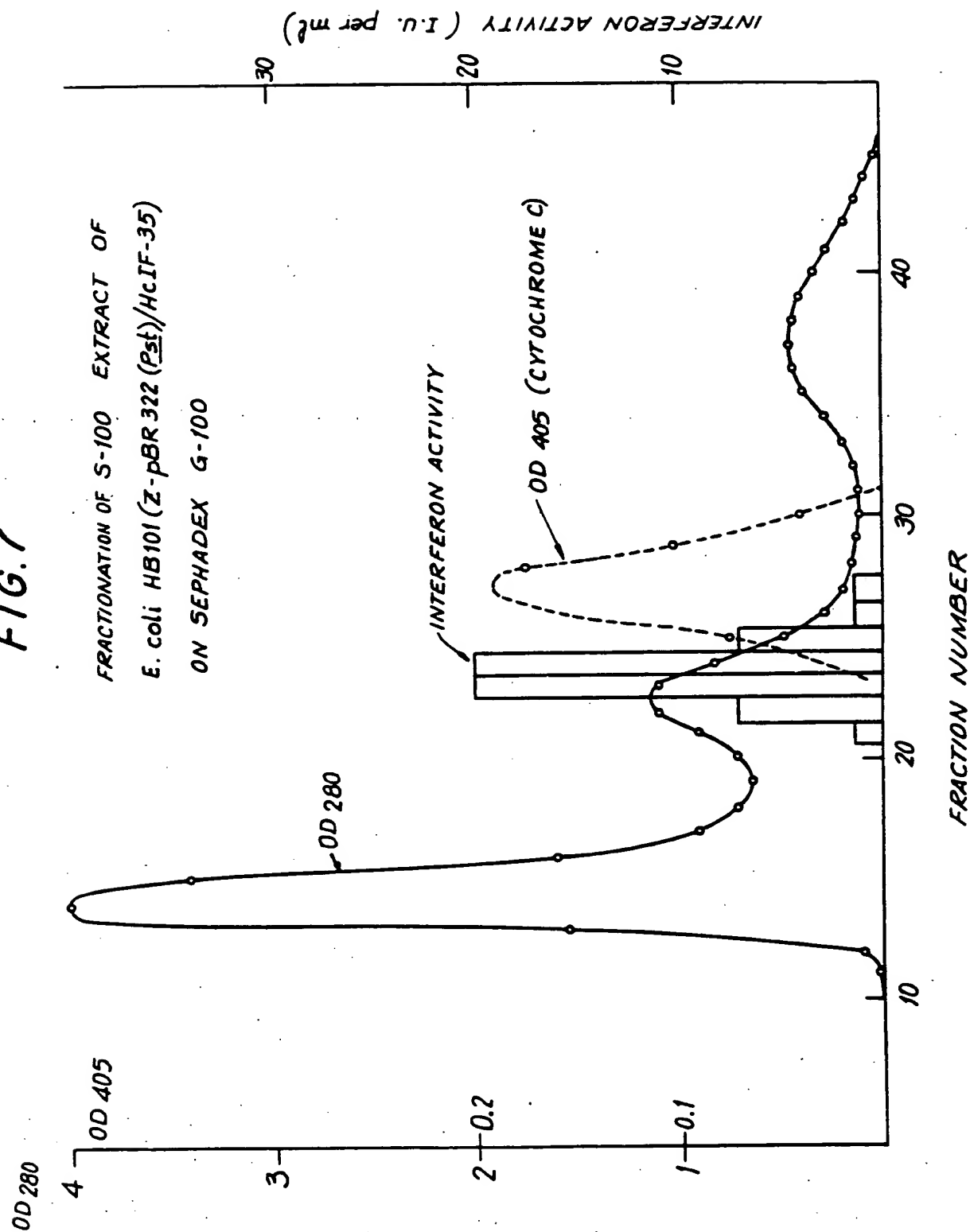
24  
 MetSerIleGlnHisPheArgValAlaLeuIleProPhePheAlaAlaPheCysLeuProValPheAlaHisArgCysSerAsn  
 24  
 pKT279 ATGAGTATTCAACATTTCCGTGTGCCCCATTATCCCTTTTGGGCAATTTTGGCTTCCCTGTTTGTCTACCCAGCAATG...  
 Pat

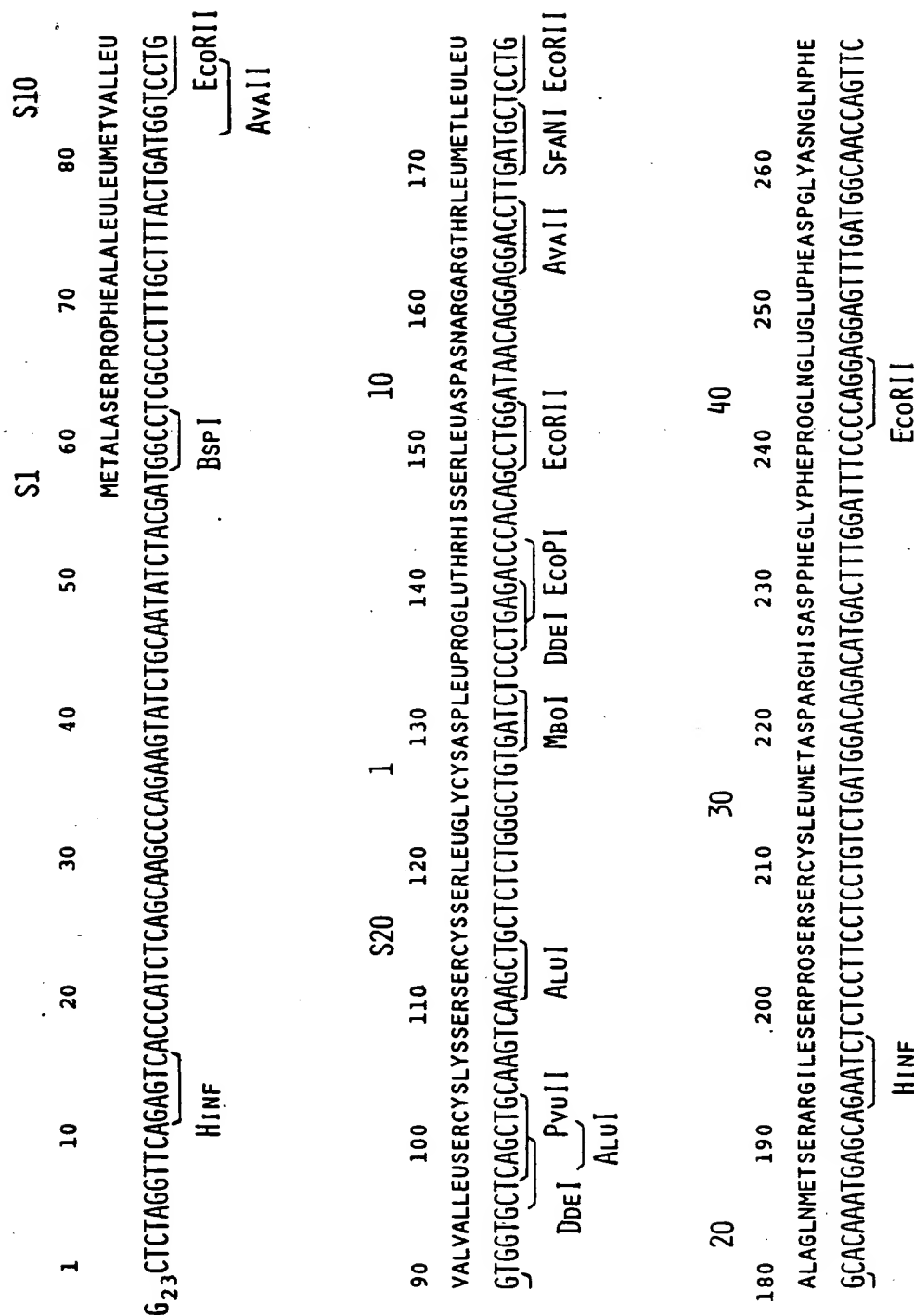
25  
 MetSerIleGlnHisPheArgValAlaLeuIleProPhePheAlaAlaPheCysLeuProValPheAlaHisProLeuGlnGln  
 25  
 pKT280 ATGAGTATTCAACATTTCCGTGTGCCCCATTATCCCTTTTGGGCAATTTTGGCTTCCCTGTTTGTCTACCCAGCAATG...  
 Pat

27  
 MetSerIleGlnHisPheArgValAlaLeuIleProPhePheAlaAlaPheCysLeuProValPheAlaHisProGluThr  
 27  
 pKT287 ATGAGTATTCAACATTTCCGTGTGCCCCATTATCCCTTTTGGGCAATTTTGGCTTCCCTGTTTGTCTACCCAGAAACG...  
 AlaAlaAlaMet  
 GCTGCAGCAATG...  
 Pat

FIG 6

FIG. 7





**FIG. 8**

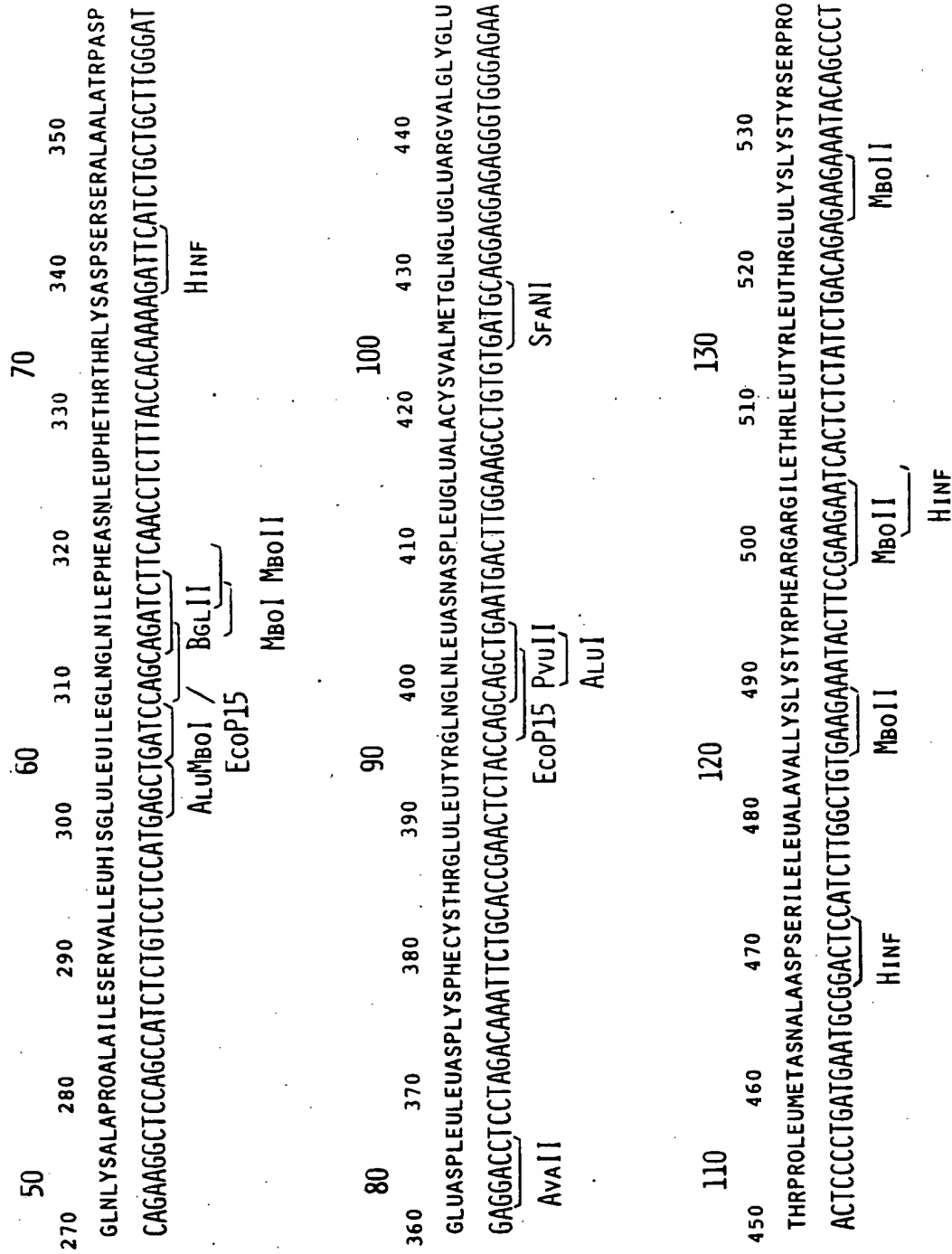


FIG.9



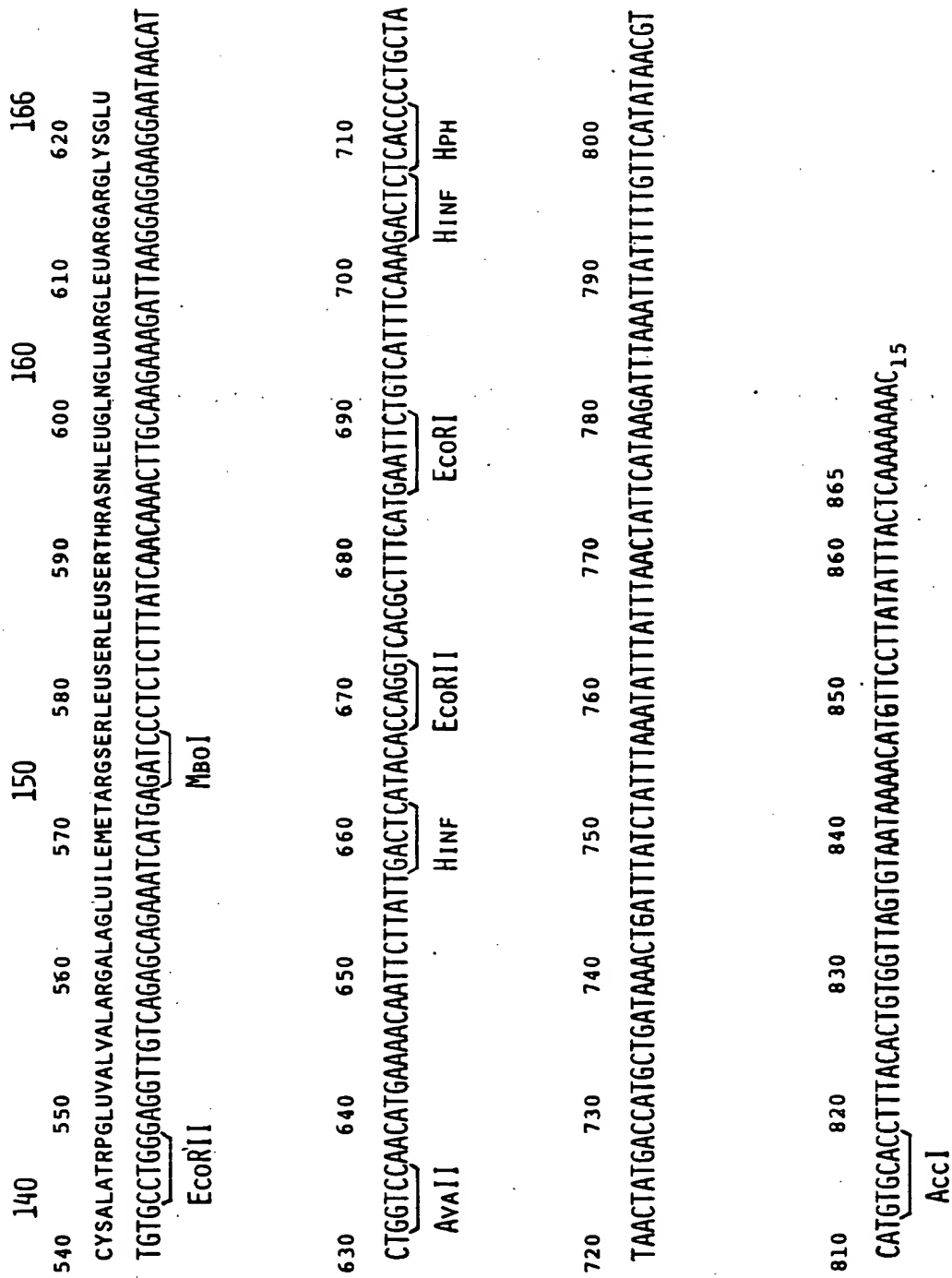
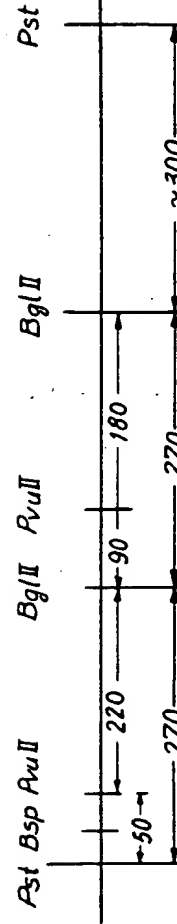
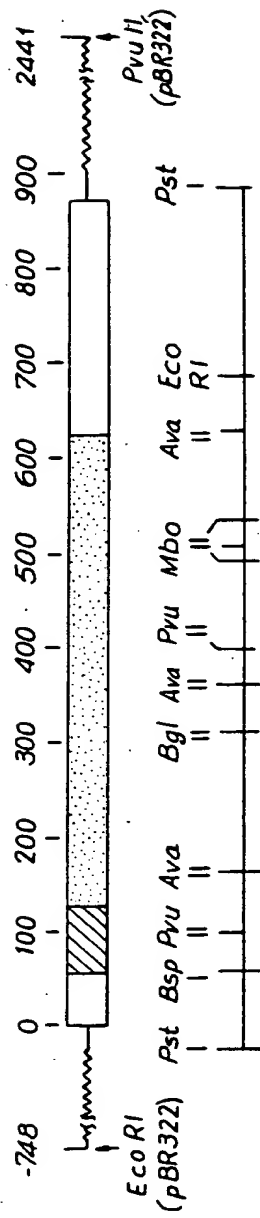


FIG. 10

FIG. II



206(11)  
 -50 -40  
 6<sub>13</sub>TTACTGGTGGCCCTC  
 leu leu val ala leu  
 -20

2H(1) met ala ser pro phe ala leu leu met val leu  
 G<sub>23</sub>CTCTAGGTTACAGATCACCCTATCTCAGCAAGCCAGAGTATCTGCAATATCTACGATGGCCCTGGCCCTTTGGCTTTACTGATGGTCTCTG  
 -120 -110 -100 -90 -80 -70 -60 -50 -40

206(11) CTGGTGCCTCAGCTGCAAGTCAAGCTGCTCTGTTGGGCTGTGATCTGCTCAAAACCCACAGCCCTGGGTAAGCAGGAGGACCCTTGATGCTCTCTG  
 leu val leu ser cys lys ser cys ser val gly cys asp leu pro gln thr his ser leu gly ser arg arg thr leu met leu leu  
 -30 -20 -10 -1 -10 10 20 30 40 50  
 -10 -1 1 10

2H(1) val val leu ser cys lys ser cys ser leu gly cys asp leu pro glu thr his ser leu asp asn arg thr leu met leu leu  
 GTGGTGCCTCAGCTGCAAGTCAAGCTGCTCTGTTGGGCTGTGATCTGCTCAAGGAGGACCCTGGGTAACAGGAGGACCCTTGATGCTCTCTG  
 -30 -20 -10 -1 10 20 30 40 50

FIG. 12

206(11) GCACAGATGAGGAGAATCCTCTTTCTCCCTGCTTGAAGGACAGACAIGACITTTGGATTTCCTCCAGGAGGAGTTT---GGCAACCAAGTTC.  
 ALA GLN MET ARG ARG ILE SER LEU PHE SER CYS LEU LYS ASP ARG HIS ASP PHE GLY PHE PRO GLN GLU PHE - GLY ASN GLN PHE

2H(1) GCACAAATGAGCAGAAATCTCTCTTCCCTGCTGATGGACAGACAIGACITTTGGATTTCCTCCAGGAGGAGTTTIGATGGCAACCAAGTTC.  
 ALA GLN MET SER ARG ILE SER PRO SER SER CYS LEU MET ASP ARG HIS ASP PHE GLY PHE PRO GLN GLU PHE ASP GLY ASN GLN PHE

206(11) CAAAGGCTGAACCATCCCTGCTCTCCATGAGATGATCCAGCAGATCTTCAATCTCTTCAGCACAAAGGACATCTGCTGCTGGGAT.  
 GLN LYS ALA GLU THR ILE PRO VAL LEU HIS GLU MET ILE GLN GLN ILE PHE ASN LEU PHE SER THR LYS ASP SER ALA ALA TRP ASP

2H(1) CAGAAGGCTCCAGGCTCTGCTCTCCATGAGCTGATCCAGCAGATCTTCAACCTCTTTIACCACAAAAGATTCATCTGCTGCTGGGAT.  
 GLN LYS ALA PRO ALA ILE SER VAL LEU HIS GLU LEU ILE GLN GLN ILE PHE ASN LEU PHE THR THR LYS ASP SER ALA ALA TRP ASP

FIG. 13

**FIG. 14**

206(11) 420 430 440 450 460 470 480 490 500  
 JGIGCCITGGGAGGTIGTCAGAGCGAGAAATCATGAGATCITTTTCTTTTGTCAACAACITGCAAGAAAGTTAAGAAGTAAGGAATGAAAA.  
 CYS ALA TRP GLU VAL VAL ARG ALA GLU ILE MET ARG SER PHE SER LEU SER THR ASN LEU GLN GLU SER LEU ARG SER LYS GLU  
 140 150 160 165

2H(1) 140 150 160 166  
 CYS ALA TRP GLU VAL VAL ARG ALA GLU ILE MET ARG SER LEU SER LEU SER THR ASN LEU GLN GLU ARG LEU ARG ARG LYS GLU  
 JGIGCCITGGGAGGTIGTCAGAGCGAGAAATCATGAGATCCCTCTCTTTATCAACAACITGCAAGAAAGATTAGGAGGAAGGAATAACAT  
 420 430 440 450 460 470 480 490 500

206(11) 510 520 530 540 550 560 570 580  
 CTGGTTCAACATGGAAATGATTTTCATTGATTGCGATGCCAGCTCACCTTTTATGA--TCIGCCATTTCAAAGACTCATGTTCIGCTA

2H(1) 510 520 530 540 550 560 570 580 590  
 CTGGTCCAACATGAAAACAATTCTTATTGACTCATACACCAGGTCAGGCTTTCATGAATTCIGCTCATCAAGAACTCTCACCCCTGCTA

FIG.15

206(11) 590 600 610 620 630 640 650 660 670 680  
TGACCATGACACGATTAAATCTTTTCAAATGTTTTAGGAGTATTAAATCAACATTGTATTCAGCTCTTAAGGCACTAGTCCCTTACAGAG

24(1) 600 610 620 630 640 650 660 670 680  
TAACATGACCATGCTGATAAACTGATTATCTATTTAAATATTTAACTATTCATAAGATTAAATTTATTTTTCATATAACGTC

206(11) 690  
GACCATGCTGAC<sub>29</sub>

24(1) 690 700 710 720 730 740  
ATGTGCACCTTTACACTGTGGTTAGTGTAAATAAACATGTTCTTATATTTACTCAAAAAAAC<sub>15</sub>

FIG. 16

FIG. 17

↑ Pvu II      ↑ Hinf      ↑ Pst I  
 ↓ Bgl II      ↓ Mbo I

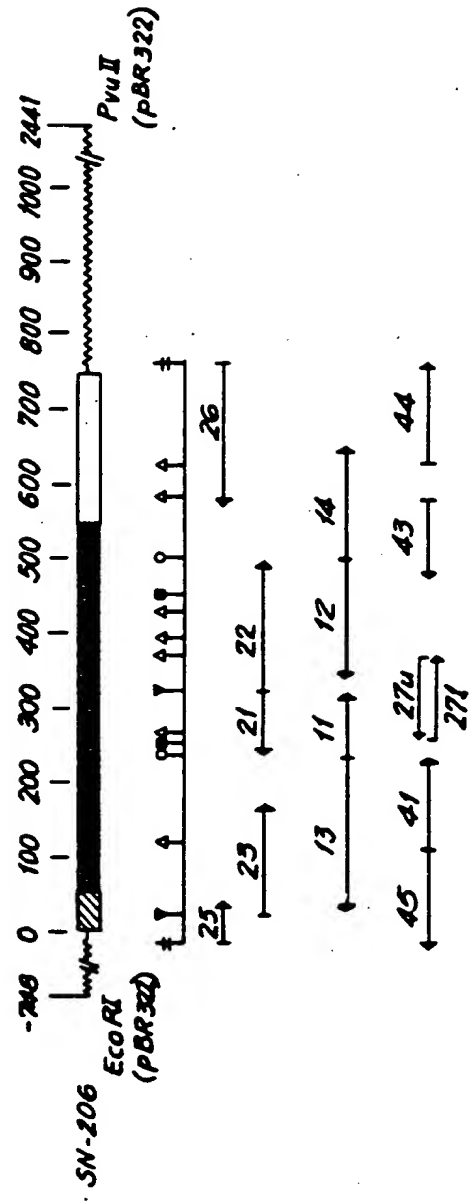
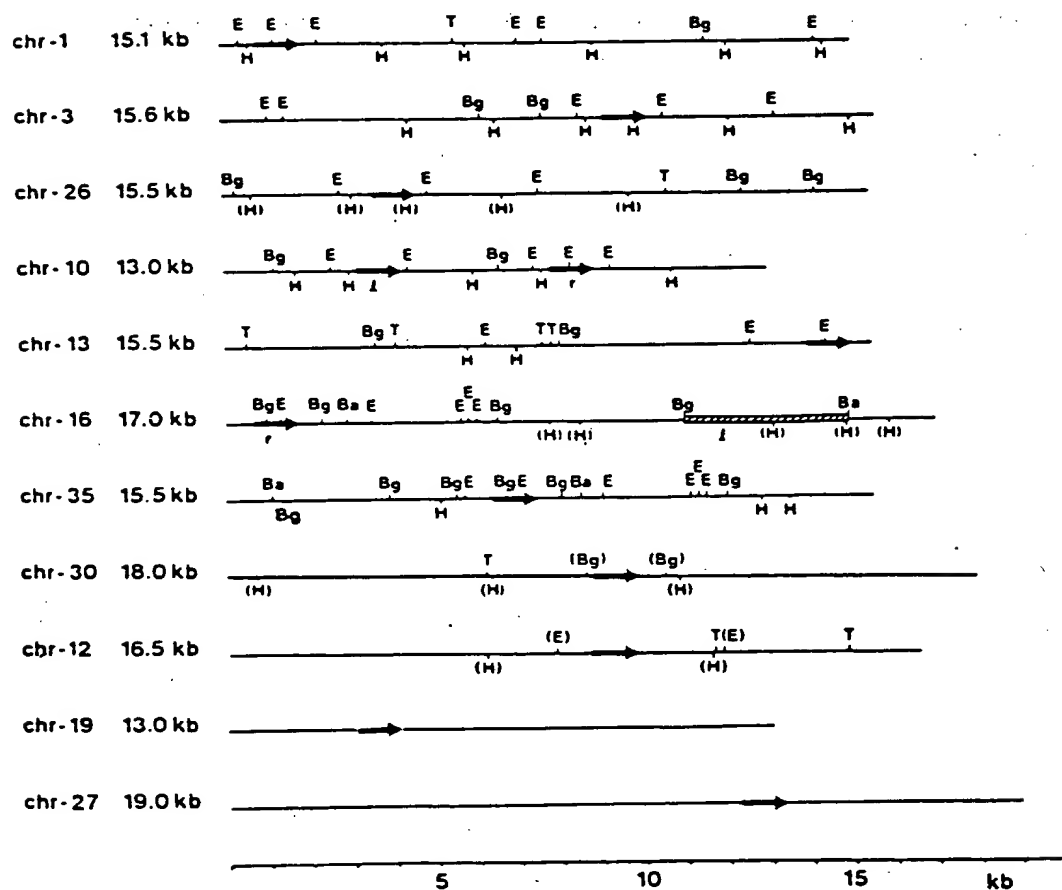




FIG.18

PARTIAL RESTRICTION MAPS OF CLONED, IFN- $\alpha$  RELATED  
CHROMOSOMAL DNA SEGMENTS



E : EcoRI, Ba : BamHI, Bg : BglII, H : HindIII, T : Tacl





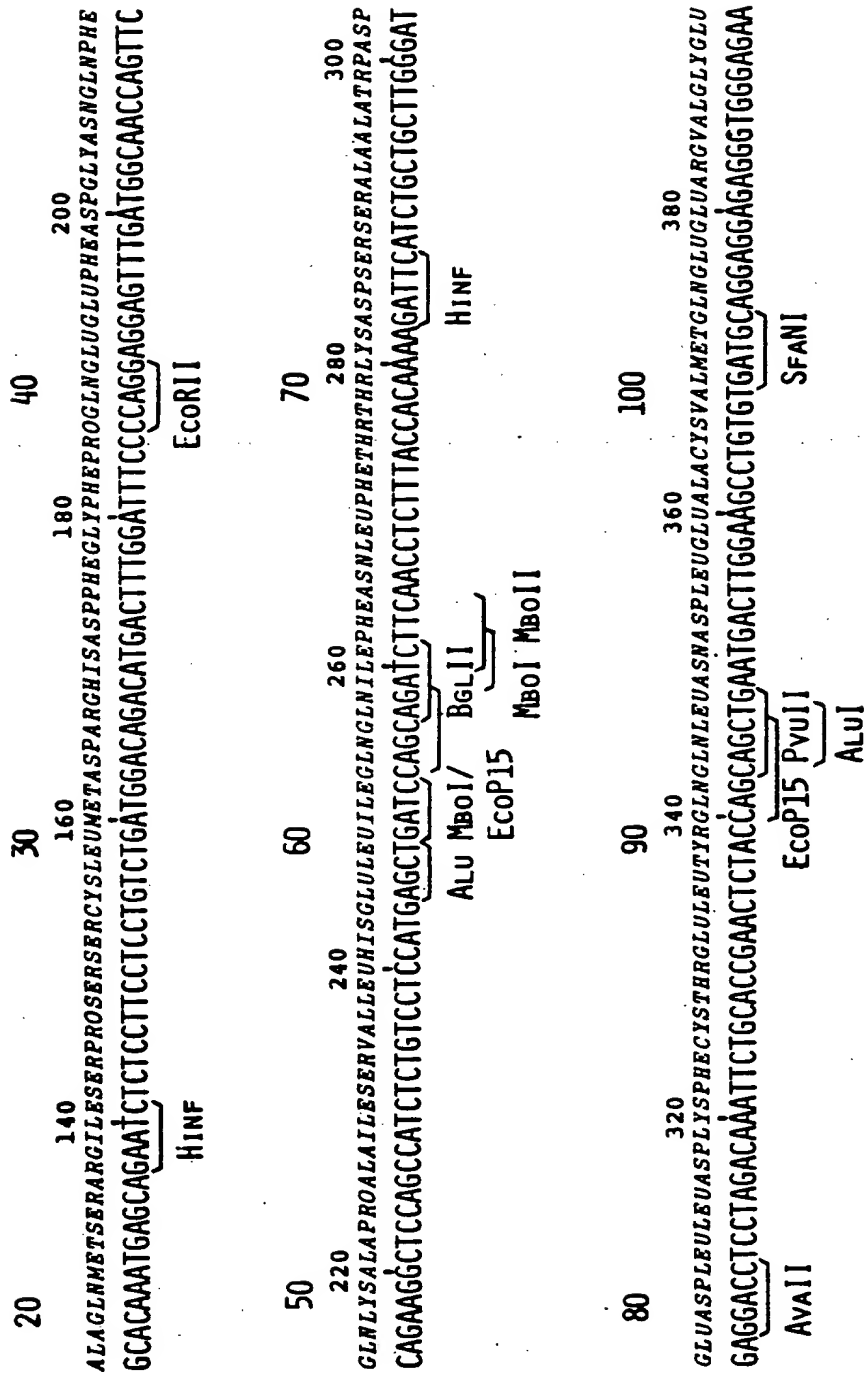


FIG. 21

110 120 130 140 150 160 166  
 400 420 440 460 480  
 THRPROLEUMETASNALAAASPSERILELEU<sup>400</sup>ALAVALLYSLYSTYRPH<sup>420</sup>EARGARGILETH<sup>440</sup>RLEUTYRLEUTH<sup>460</sup>RGLULYSLYSTYRSERPRO<sup>480</sup>  
 ACTCCCTGATGAATGGGACTCCATCTTGGCTGTGAAGAAATACTCCGAAGATCACTCTCTATCTGACAGAGAAGAAATACAGCCCT  
 HINF MboII HINF MboII  
 110 120 130 140 150 160 166  
 400 420 440 460 480  
 CYSALATRPGLUVALVARGALAGLUILEMETARGSERLEUSERLEUSERTHRASNLEUGLNGLUARGLEUARGGLYSGLU  
 TGTGCTGGGAGGTTGT<sup>500</sup>CAGAGCAGAAATCATGAGATCCCTCTCTTTATCAACAACTTGAAGAAGATTAAAGGAGGAAGGAATAACAT<sup>560</sup>  
 EcoRI MboI  
 580 600 620 640 660  
 CTGGTCC<sup>580</sup>AACATGAAACAATTCTTATTTGACTCATACACCGGTCA<sup>600</sup>CGCTTTCATGAATTCGTCA<sup>620</sup>TTTCAAGACTCTCACCCCTGCTA<sup>660</sup>  
 A<sup>600</sup>all HINF EcoRI HINF HPH  
 680 700 720 740  
 TAACTATGACCATGCTGATAAACTGATTATCTATTAAATATTATTAACTATTCAAGATTAAATATTTTGTTCATATAACGT  
 760 780 800 820 840  
 CATGIGCAGCTTACACTGIGGTTAGTGTAAATAAACAATGTTCCCTTATATTIACICCAATCCATTATTTGTGTTGTTCAATAACTTTTA  
 HgIA

FIG. 22

860 880 900 920  
CTATAGGAACTTCCTGTAATGTTTCATTCTTTAATAATGAATTCCTAGCCTGACTGTGCAACCTGATTAGAGAAATAAAGGGTATATTTTA

940 959  
TTTGCTTATCATTATTATAIGTAAGA

FIG.23

FIG. 24

LINKAGE OF IFN- $\alpha$  RELATED GENES

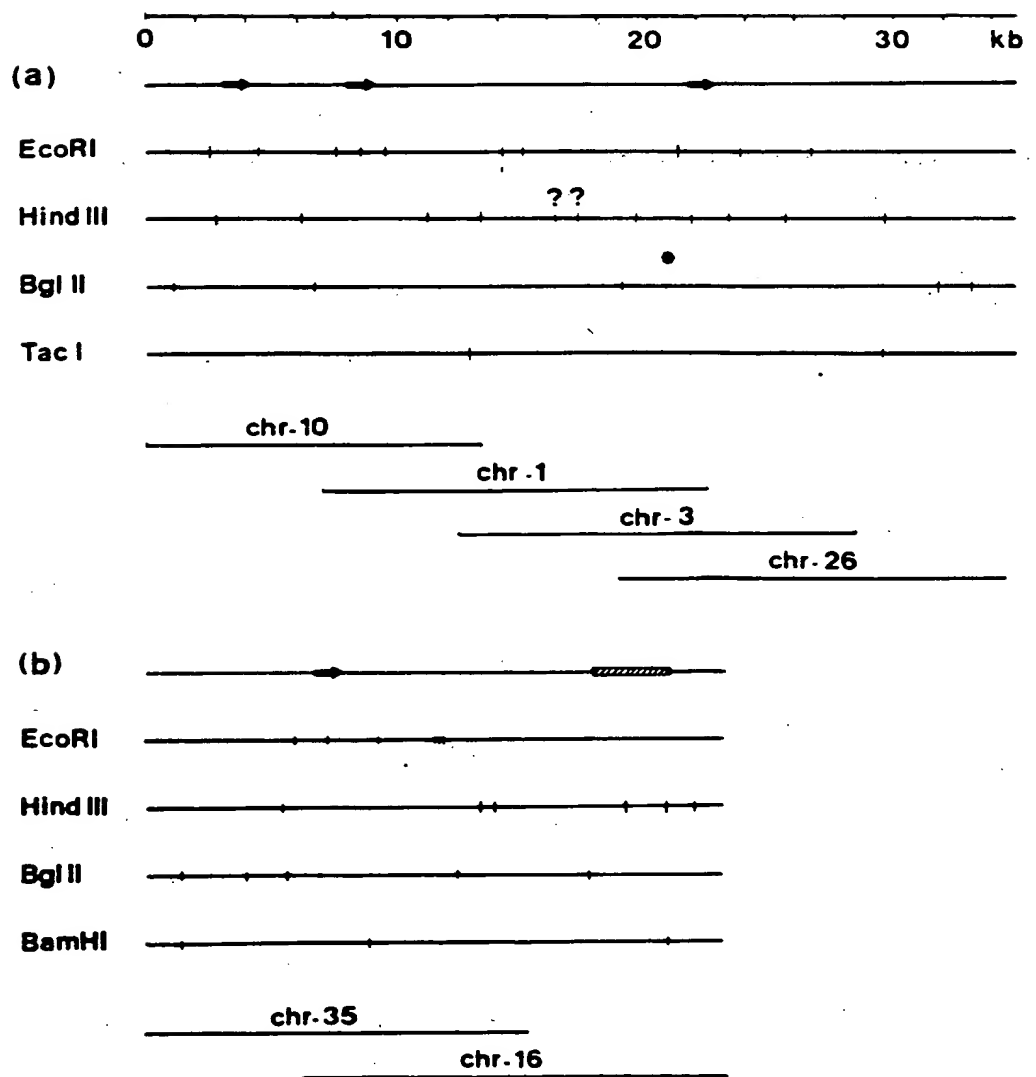


FIG. 25

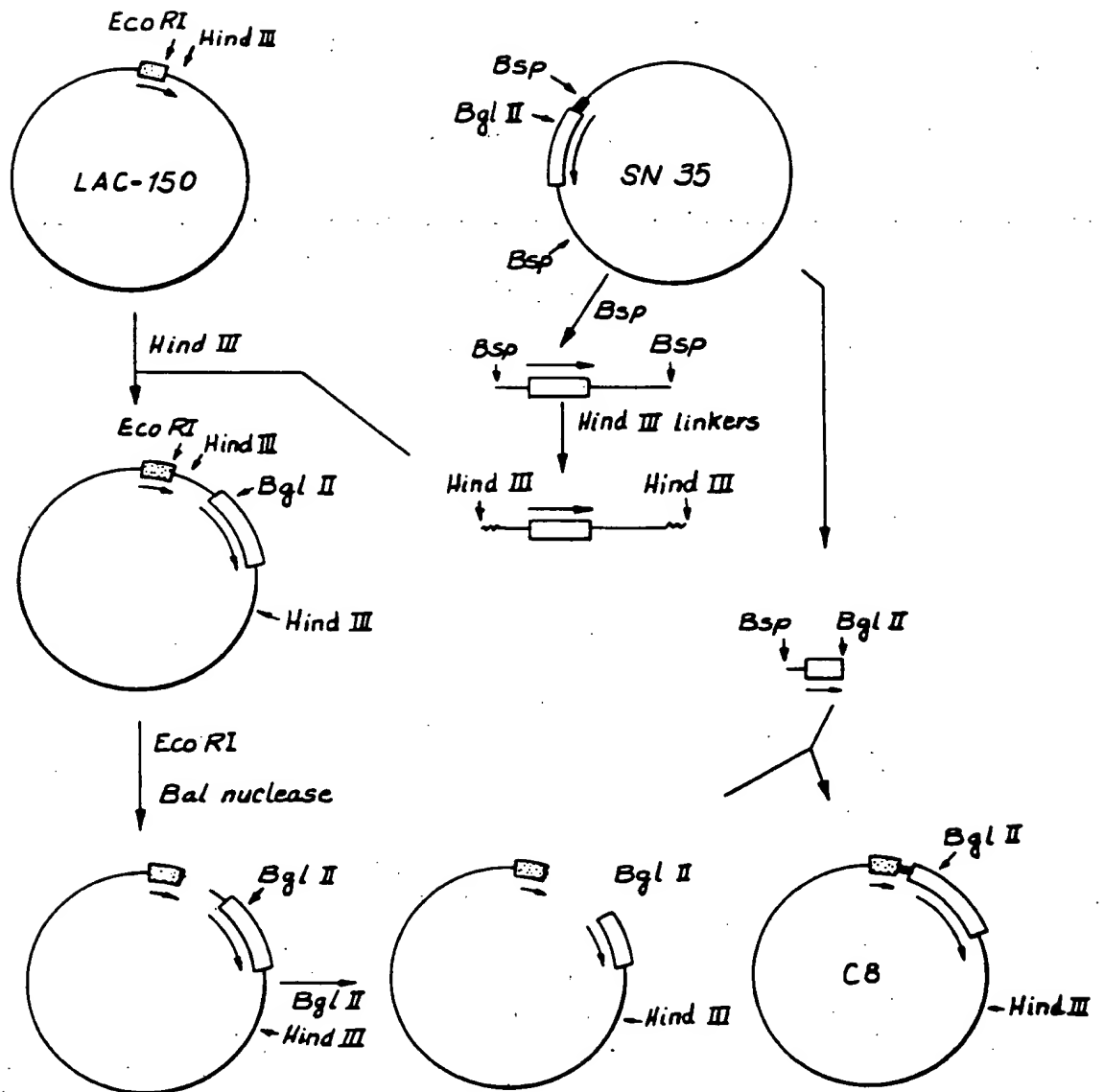




FIG. 26

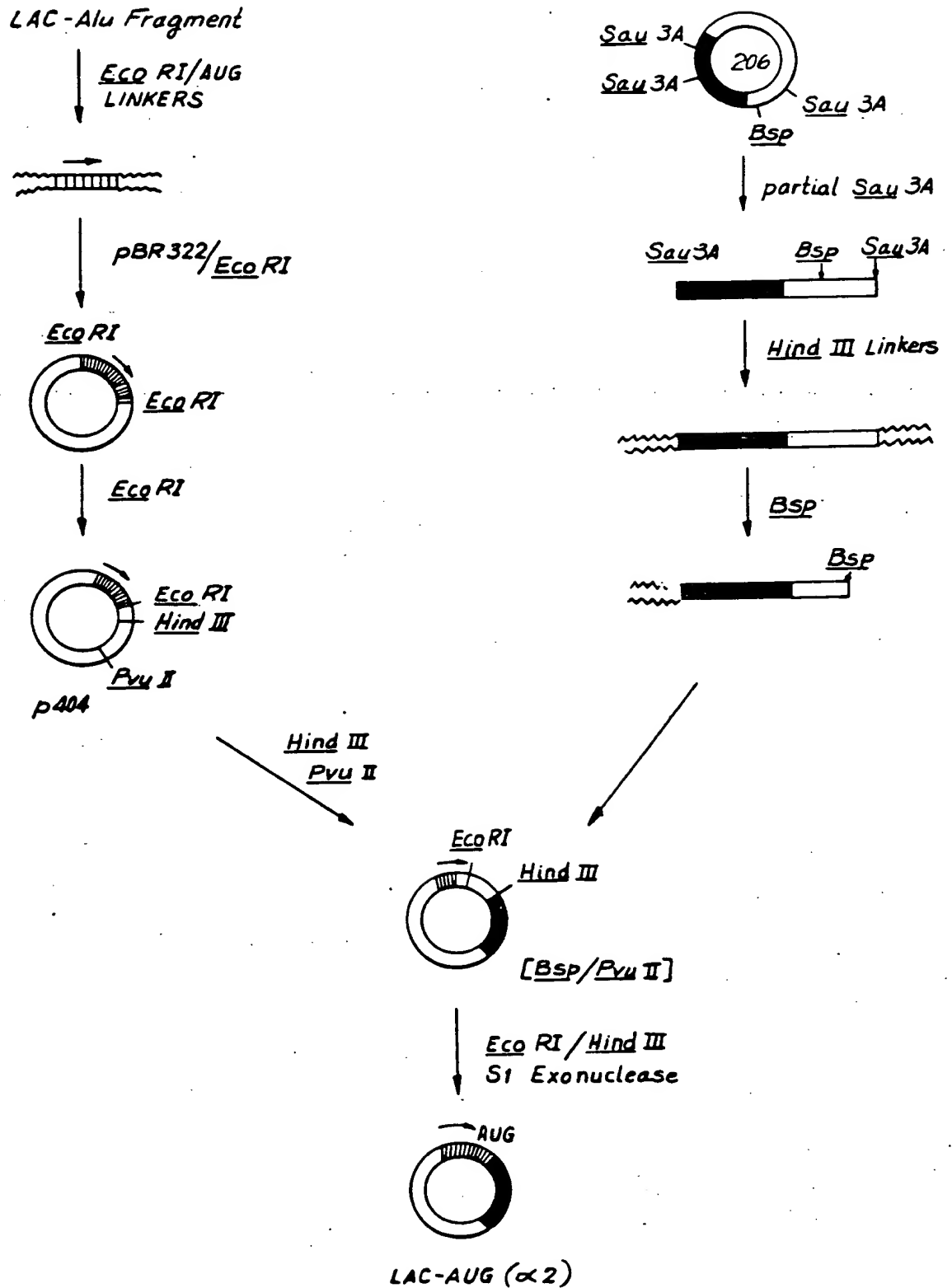


FIG. 27

CONSTRUCTION OF PLASMID LAC-AUG ( $\alpha$ -2)

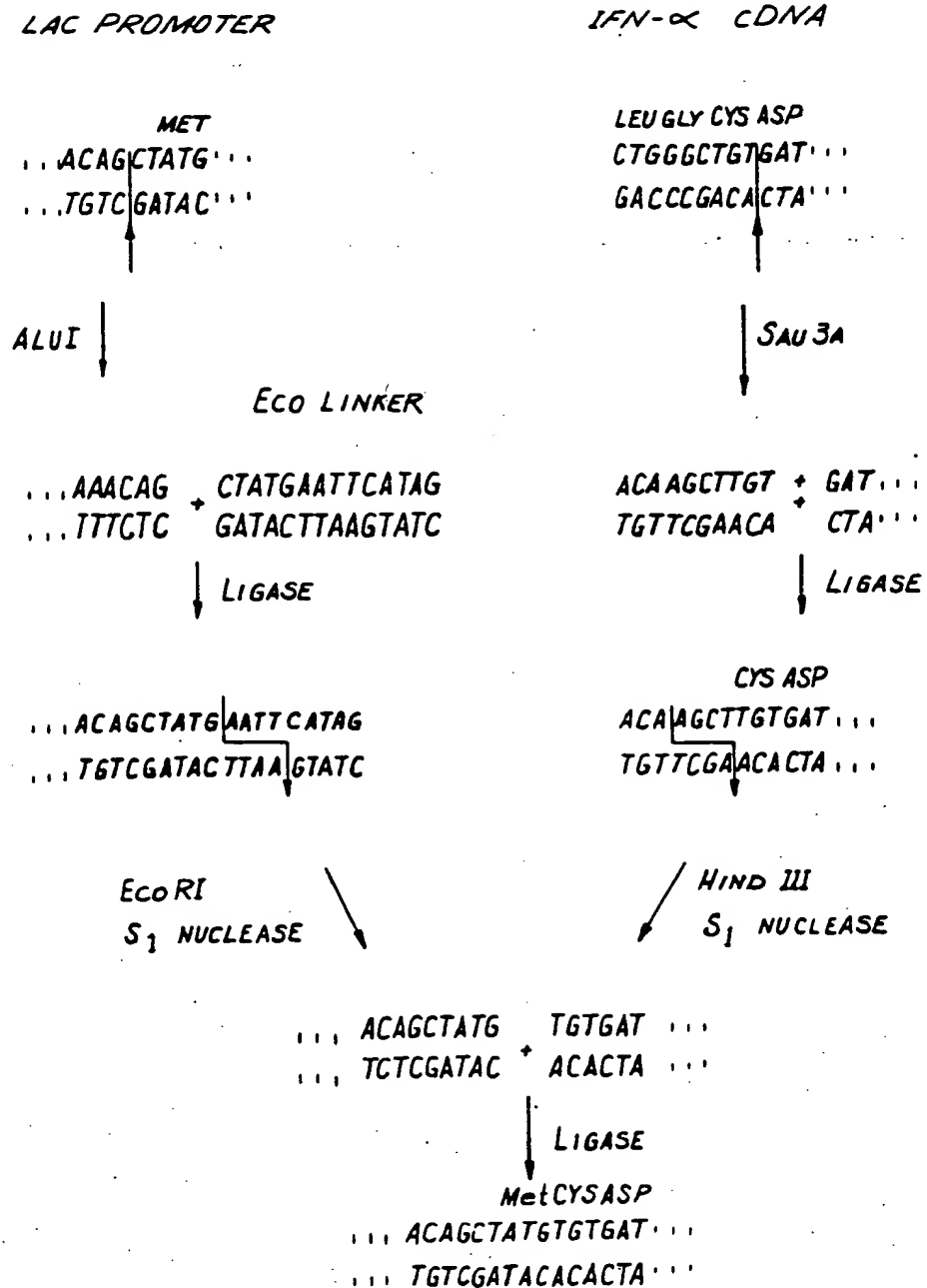
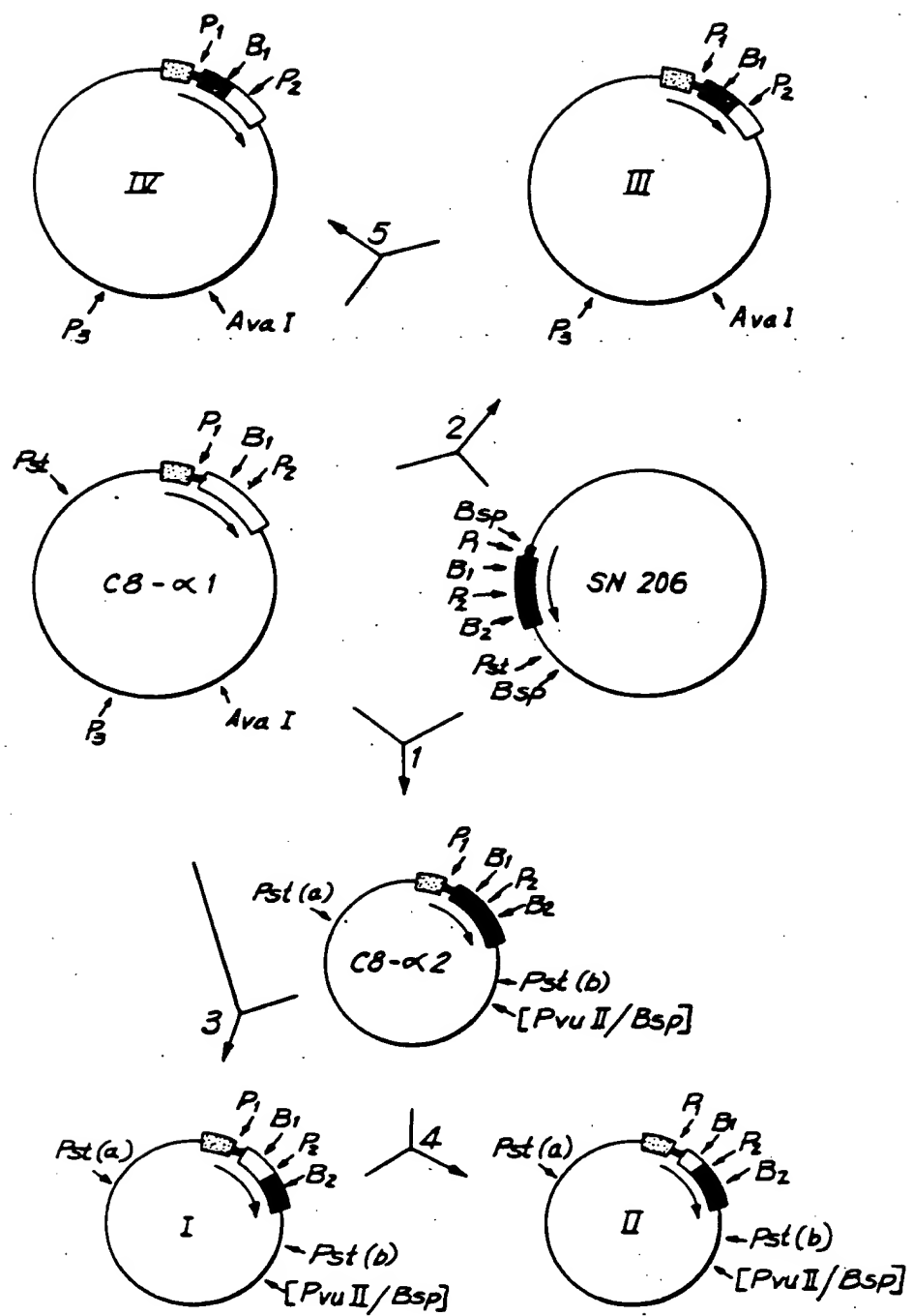


FIG. 28



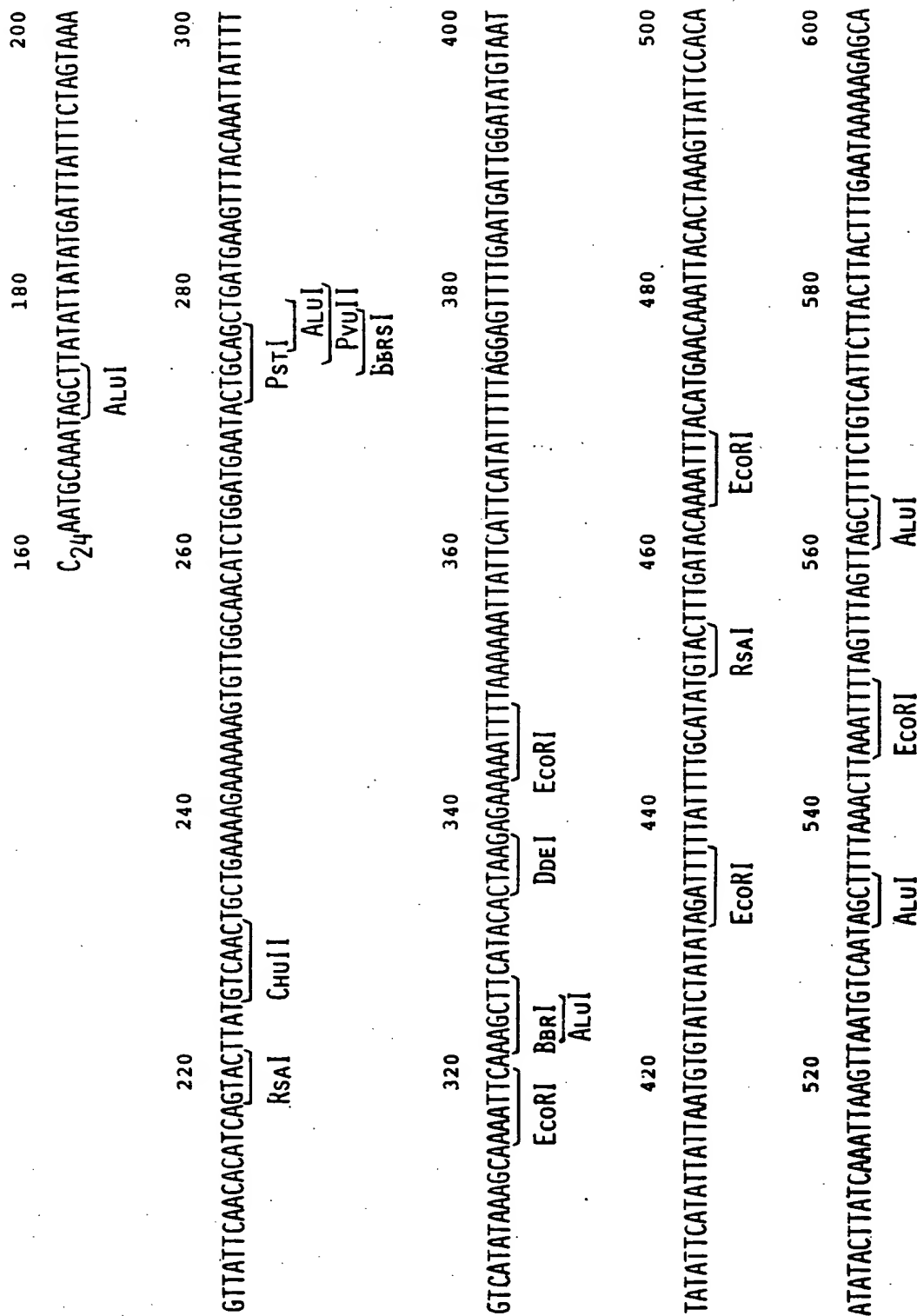


FIG. 29

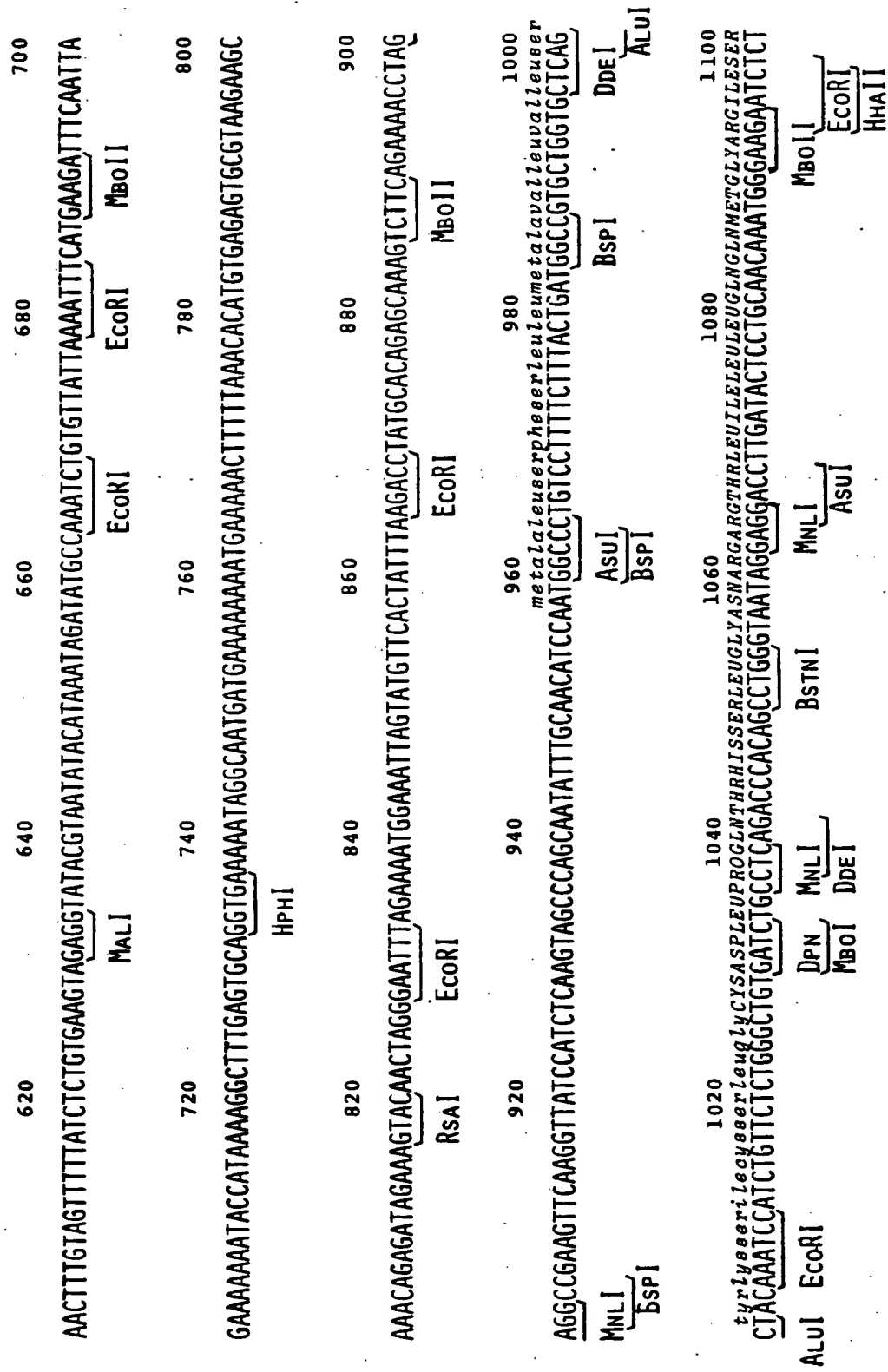


FIG. 30

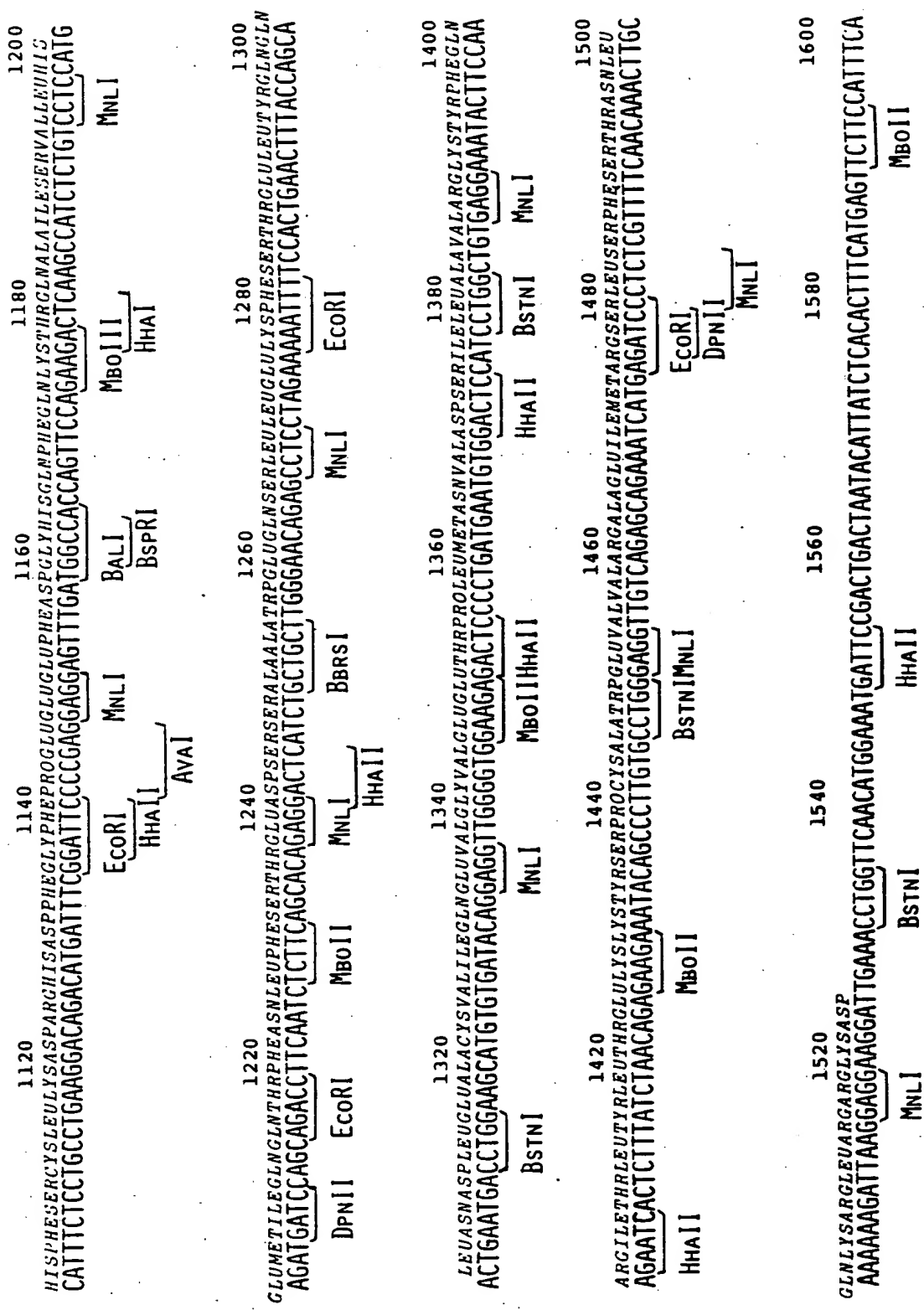


FIG. 31

